

AMENDMENTS TO THE CLAIMS:

Claims 5 and 35-40 are cancelled. Claims 41-57 are added. The following is the status of the claims of the above-captioned application, as amended.

Claims 1-40 (Cancelled.)

41. (New.) A method of constructing a variant of a parent maltogenic alpha-amylase, wherein said parent maltogenic alpha-amylase has an amino acid sequence which is at least 70% identical to amino acid residues 1-686 of SEQ ID NO:2, and wherein said parent maltogenic alpha-amylase has an active site which comprises a cluster of three amino acid residues corresponding to positions D329, D228 and E256 in SEQ ID NO:2, which method comprises:

- a) modeling the parent alpha-amylase on the three-dimensional structure of amino acid residues 1-686 of SEQ ID NO:2 depicted in the Appendix to produce a three-dimensional structure of the parent alpha-amylase;
- b) identifying in said three-dimensional structure of the parent alpha-amylase an amino acid residue which (i) is within 15 Å of one of said three amino acid residues and (ii) is involved in electrostatic or hydrophobic interactions with an active site residue; and
- c) constructing the variant by substituting the amino acid residue identified in said b) with another amino acid residue which changes the electrostatic and/or hydrophobic surroundings of said active site residue, and which can be accommodated in the structure.

42. (New.) The method of claim 41, wherein said b) comprises identifying in said three-dimensional structure of the parent alpha-amylase an amino acid residue which (i) is within 10 Å of one of said three amino acid residues and (ii) is involved in electrostatic or hydrophobic interactions with an active site residue.

43. (New.) The method of claim 41, wherein the method further comprises

- d) testing the pH dependent activity of said variant constructed in said c); and
- e) selecting a variant having an altered pH dependent activity as compared to the parent amylase.

44. (New.) The method of claim 41, wherein said parent maltogenic alpha-amylase is at least 80% identical to amino acid residues 1-686 of SEQ ID NO:2.

45. (New.) The method of claim 41, wherein said parent maltogenic alpha-amylase is at least 90% identical to amino acid residues 1-686 of SEQ ID NO:2.
46. (New.) The method of claim 41, wherein said parent maltogenic alpha-amylase is at least 95% identical to amino acid residues 1-686 of SEQ ID NO:2.
47. (New.) The method of claim 41, wherein said parent maltogenic alpha-amylase is at least 98% identical to amino acid residues 1-686 of SEQ ID NO:2.
48. (New.) The method of claim 41, wherein said parent maltogenic alpha-amylase has the amino acid sequence of amino acid residues 1-686 of SEQ ID NO:2.
49. (New.) The method of claim 42, wherein said parent maltogenic alpha-amylase is at least 80% identical to amino acid residues 1-686 of SEQ ID NO:2.
50. (New.) The method of claim 42, wherein said parent maltogenic alpha-amylase is at least 90% identical to amino acid residues 1-686 of SEQ ID NO:2.
51. (New.) The method of claim 42, wherein said parent maltogenic alpha-amylase is at least 95% identical to amino acid residues 1-686 of SEQ ID NO:2.
52. (New.) The method of claim 42, wherein said parent maltogenic alpha-amylase is at least 98% identical to amino acid residues 1-686 of SEQ ID NO:2.
53. (New.) The method of claim 42, wherein said parent maltogenic alpha-amylase has the amino acid sequence of amino acid residues 1-686 of SEQ ID NO:2.
54. (New.) The method of claim 41, wherein the method comprises repeating steps b) and c) recursively.
55. (New.) The method of claim 41, wherein the method further comprises
d) repeating steps b) and c) recursively;
e) preparing the variant resulting from steps a) – d);

- f) testing the pH dependent activity of said variant; and
- g) selecting a variant having an altered pH dependent activity as compared to the parent amylase.

56. (New.) The method of claim 41, wherein the method further comprises
- d) repeating steps b) and c) recursively;
 - e) making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than c),
 - f) preparing the variant resulting from steps a) – e);
 - g) testing the pH dependent activity of said variant; and
 - h) selecting a variant having an altered pH dependent activity as compared to the parent amylase.
57. (New.) The method of claim 41, wherein the method further comprises:
- d) repeating steps b) and c) recursively;
 - e) making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than c),
 - f) preparing the variant resulting from steps a) – e);
 - g) testing the pH dependent activity of said variant;
 - h) repeating steps a) - g) recursively; and
 - i) selecting a variant having an altered pH dependent activity as compared to the parent amylase.